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#10

600-1-266

FIGURE 1A

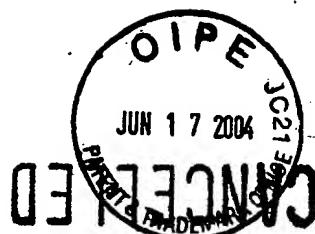
SEQ ID NO:1



600-1-266. FIGURE 1B

SEQ ID NO:2

Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
1 5 10 15
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val
20 25 30
Asn Leu Ser His Leu Asp Gly Asn Leu Ser Asp Pro Cys Gly Pro Asn
35 40 45
Arg Thr Asn Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
50 55 60
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
65 70 75 80
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
85 90 95
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
100 105 110
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val
115 120 125
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile
130 135 140
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu
145 150 155 160
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys
165 170 175
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys
180 185 190
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala
195 200 205
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser
210 215 220
His Pro Thr Trp Tyr Trp Glu Asn Leu Val Lys Ile Cys Val Phe Ile
225 230 235 240
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu
245 250 255
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu
260 265 270
Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
275 280 285
Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
290 295 300
Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
305 310 315 320
His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
325 330 335
Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
340 345 350
Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
355 360 365
Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
370 375 380
Thr Asn His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
385 390 395 400



600-1-266-

FIGURE 2A

SEQ ID NO:3

1 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcggtccc ctccgcctga
61 cgctcctctc tgtctcagcc aggactggtt tctgtaaagaa acagcaggag ctgtggcagc
121 ggcgaaagga agcggctgag ggcgttggaa cccgaaaagt ctcggtgctc ctggctaccc
181 cgcacagcgg tgcccgcgg gccgtcagta ccatggacag cagcgtgccc cccacgaacg
241 ccagcaattg cactgatgcc ttggcgtact caagttgcgc cccagcaccc agccccggtt
301 cctgggtcaa cttgtcccac tttagatggca acctgtccga cccatgcggc cccgaaacggca
361 ccaacctggg cgggagagac agcctgtgcc ctccgaccgg cagtccttcc atgatcacgg
421 ccatcacatcgtatggccctc tactccatcg tgtgcgtggt ggggtcttc gggaaacttcc
481 tggtcatgta tgtgattgtc agatacacca agatgaagac tgccaccaac atctacattt
541 tcaaccttgc tctggcagat gccttagcca ccagtacccct gcccattccag agtgtqaatt
601 acctaataatggg aacatggcca tttgaacca tcctttgcaaa gatagtgatc tccatagatt
661 actataacat gttcaccagc atattcaccc tctgcaccat gagtgttgcgat cgatacattt
721 cagtcgtccca ccctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca
781 atgtctgcaatctggatccctc tcttcagcca ttgggtttcc tgaatgttc atggctacaa
841 caaaataacag gcaagggttcc atagattgtc cactaacatt ctctcatccaa acctggtaact
901 gggaaaacct cgtgaagatc tgtgtttca tcttcgcctt cattatgccca gtgctcatca
961 ttaccgtgtc ctatggactg atgatcttgc gcctcaagag tgcgtccatg ctctctggct
1021 ccaaagaaaa ggacaggaat cttcgaagga tcaccaggat ggtgtgggt gtgggtggctg
1081 tggtcatcgt ctgctggact cccattcaca tttacgtcat cattaaagcc ttgggttacaa
1141 tcccagaaac tacgttccag actgtttctt ggcacttctg cattgtctca gttacacaaa
1201 acagctgcct caacccagtc ctatgtcat ttctggatga aaacttcaaa cgatgtttca
1261 gagagttctg tatcccaacc ttttccaaaca ttgagcaaca aaactccact cgaattcgtc
1321 agaacactag agaccacccc tccacggcca atacagtggta tagaactaat catcagctag
1381 aaaatctgga agcagaaaact gtcgggttgc cctaaacaggg tctcatgcca ttccgaccc
1441 caccaagctt agaagccacc atgtatgtgg aagcaggttgc ttcaagaat gtgttaggagg
1501 ctctaattct cttagggaaagt gcctactttt aggtcatccaa acctctttcc tctctggcca
1561 ctctgtctg cacatttagag ggacagccaa aagtaagtgg agcatttggaa aggaaaggaa
1621 tataccacac cgaggagtcc agtttgtcag aagcacccag tggaaaccaaa accccatctg
1681 gtatgtgaat tgaagtcatc ataaaaggtg acccttctgt ctgtaaagatt ttatccaa
1741 gcaaataattt atgacatcaa caaagaagaa ccatcttttgc ttaagttcac cgttagtaaca
1801 catabaaatgaa atgtctaccc tgcataaagc accttgaatg gaaggtccga gtcttttttag
1861 tgggtttgc agggaaatgaa tccattatttc tatttttagac ttttaacttc aacttaaaat
1921 tagcatctgg ctaaggcattt attttccatc ccatttcttgc gttttgtatt gttaaaaaaa
1981 aataacatct ctttcatctc gctccataat tgcaagggaa gagattagca tgaaaggtaa
2041 tctgaaacac agtcatgtgt canctgtaga aaggttgatt ctcatgcact ncaaataactt
2101 ccaaagagtc atcatggggg attttcattt cttaggcttt cagtgggttgc ttccctggaaat
2161 tc



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FIGURE 2B

SEQ ID NO:4

Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
1 5 10 15
Leu Ala Tyr Ser Ser Cys Pro Pro Ala Pro Ser Pro Gly Ser Trp Val
20 25 30
Asn Leu Ser His Leu Asp Gly Asn Leu Ser Asp Pro Cys Gly Pro Asn
35 40 45
Arg Thr Asn Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
50 55 60
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
65 70 75 80
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
85 90 95
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
100 105 110
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val
115 120 125
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile
130 135 140
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu
145 150 155 160
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys
165 170 175
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys
180 185 190
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala
195 200 205
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser
210 215 220
His Pro Thr Trp Tyr Trp Glu Asn Leu Val Lys Ile Cys Val Phe Ile
225 230 235 240
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu
245 250 255
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu
260 265 270
Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
275 280 285
Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
290 295 300
Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
305 310 315 320
His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
325 330 335
Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
340 345 350
Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
355 360 365
Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
370 375 380
Thr Asn His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
385 390 395 400



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FIGURE 3A

SEQ ID NO: 5



600-1-266' FIGURE 3B
SEQ ID NO:6

Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
1 5 10 15
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val
20 25 30
Asn Leu Ser His Leu Asp Gly Asn Leu Thr Asp Pro Cys Gly Pro Asn
35 40 45
Arg Thr Asn Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
50 55 60
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
65 70 75 80
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
85 90 95
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
100 105 110
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val
115 120 125
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile
130 135 140
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu
145 150 155 160
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys
165 170 175
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys
180 185 190
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala
195 200 205
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser
210 215 220
His Pro Thr Trp Tyr Trp Glu Asn Leu Val Lys Ile Cys Val Phe Ile
225 230 235 240
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu
245 250 255
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu
260 265 270
Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
275 280 285
Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
290 295 300
Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
305 310 315 320
His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
325 330 335
Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
340 345 350
Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
355 360 365
Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
370 375 380
Thr Asn His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
385 390 395 400



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FIGURE 4

SEQ ID NO: 7

1 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcggtccc ctccgcgg
61 cgctcctctc tgttcagcc aggactgggt tctgtaaagaa acagcaggag ctgtggcagg
121 ggcgaaaggaa agcggtcgag gcgcttggaa cccgaaaagt ctcgggtctc ctggctaccc
181 cgcacagcgg tgcggcccg gccgtcagta ccatggacag cagcgtgcc cccacgaaac
241 ccagcaattt cactgatgcc ttggcgtaact caagttgtctc cccagcaccc agccccgggg
301 cctgggtcaa cttgtccac ttagatggca acctgtccga cccatgcgggt ccgaaccgca
361 ccaatctggg cgggagagac agcctgtgcc ctccgaccgg cagtccttcc atgatcacgg
421 ccatcacgt catggccctc tactccatcg tgtcggtgg ggggtcttcc ggaacttcc
481 tggtcatgtt tggattgtc agatacacca agatgaagac tgccaccaac atctacattt
541 tcaaccttgc tctggcagat gccttagcca ccagtagccct gccccttccag agtgtgaattt
601 acctaattggg aacatggca tttggaaacca tcctttgcaa gatagtgtac tccatagattt
661 actataacat gttcaccaggc atattcaccc tctgcaccat gagggtgtat cgatacattt
721 cagtctgcca ccctgtcaag gccttagatt tccgtactcc cggaaatgtcc aaaattatca
781 atgtctgcaa ctggatcctc tttcagccca ttgggtttcc tgtaatgttc atggctaccaa
841 caaaatacag gcaagggttcc atagattgtt cactaaccatt ctctcatcca acctgggtact
901 gggaaaacct cgtgaagatc tgggttttca ttttgcctt cattatgcca gtgctcatca
961 ttaccgtgtt ctatggactg atgatcttgc gcctcaagag tggccgtatg ctctctggct
1021 ccaaagaaaa ggacaggaat ctgcgaaggaa tcaccaggat ggtcggtgg gttggggctg
1081 tggtcatgtt ctgctggact cccattcaca tttacgtcat cattaaagcc ttggttaccaa
1141 tccccagaaac tacgttccag actgtttctt ggcacttctg cattgtctata gtttaccaa
1201 acagctgcct caaccaggc ttttatgtat ttctggatga aaacttcaaa cgatgttca
1261 gagagttctg tatcccaacc ttttccaaca ttgagcaaca aaactccact cgaattgtc
1321 agaacaactag agaccacccc tccacggcca atacagtgg tagaactaat catcagctag
1381 aaaatctggg agcagaaaact gtcgggttgc ccttaacaggg ttcgtaccca ttccggaccc
1441 caccaggctt agaaggccacc atgtatgtgg aagcagggttgc cttcaagaat gtgttaggagg
1501 ctcttaattctt ctagggaaagt gcctactttt aggtcatcca accttttcc tctctggcca
1561 ctctgtctg cacatttagag ggacagccaa aagtaagtgg agcatttggg agggaaaggaa
1621 tataccacac cgaggagtcc agtttgcagaa agacaccccg tggaaacccaa acccatcggt
1681 gtatgtgaat tgaagtcatc ataaaagggtt acccttctgt ctgtaaagatt ttatattca
1741 gcaaataattt atgacactcaa caaagaagaa ccatttttgc tttagttcac cgttagtaaca
1801 cattaaagttt atgctaccc tggatcaaaaggc accttgcatttq gaaagggtccga gtcttttag
1861 tggggatggaa tccatttattt tatttttagac ttttaacttc aactttaaaat
1921 tagcatctgg ctaaggcattt attttgcattt ccatttttgc gttttgtatt gtttttttttt
1981 aataacatctt ctttcatctt gtcggccatattt tgcaagggaa gagatttagca tgaaaggtaa
2041 tctgaaacac agtcatgtgtt canctgttgc aaggttgatt ctcgtacact ncaaataactt
2101 ccaaagagtc atcatggggg atttttcattt ctttaggctttt cagtggttttgc ttcctggaaat
2161 tc



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FIGURE 5

SEQ ID NO:8

1 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcggtccc ctcgcctga
61 cgctcccttc tgcgtcagcc aggactggtt tctgtaaagaa acagcaggag ctgtggcagc
121 ggcgaaagga agcggctgag ggcgttggaa cccgaaaagt ctcgggtctc ctggctaccc
181 cgcacagcgg tgcggcccg gccgtcagta ccatggacag cagcgtgccc cccacgaacg
241 ccagaatttgcactgtatgcc ttggcgtact caagttgtctc cccagcaccc agccccgggt
301 cctgggtcaa cttgtccac ttagatggca acctgtccga cccatgcggg cggaaaccgca
361 ccaacctggg cgggagagac agcctatgcc ctccgaccgg cagtcctcc atgatcacgg
421 ccatcacatcatggccctc tactccatcg tgcgttgcgttggggcttcc ggaaacttcc
481 tggtcatgtatgttgc agatacacca agatgaagac tgccaccaac atctacattt
541 tcaaccttgc tctggcagat gccttagcca ccagtacccct gccttccag agtgtgaatt
601 acctaattggg aacatggcca tttggaaacca tcccttgcac gatagtgtatccatagatt
661 actataacat gttcaccatgc atattcaccat tctgcacccat gatgttgcgttgcgatcatgt
721 cagtcgtccca ccctgtcaag gccttagatt tccgtactcc cccaaatgtcc aaaattatca
781 atgttcgtcaa ctggatccctc tcttcagcca ttggcttcc tggatgttgc atggctacaa
841 caaaatacag gcaagggttcc atagattgtatca cactaacatt ctctcatccaa acctggtact
901 gggaaaacccct cgtgaagatc tgcgtttca tcttcgcctt cattatgcca gtgtcatca
961 ttaccgtgtctatggactg atgatcttgc gcctcaagag tgcgttgcgttgc ctctctggct
1021 ccaaagaaaa ggacaggaat ttgcgaagga tcaccaggat ggtgtgggtg gtgggtggctg
1081 tggatgtatctgt ctgtggact cccattcaca ttgcgttgc cattaaagcc ttgggttacaa
1141 tcccaagaaac tacgttccag actgtttctt ggacttgc tattgtctca gtttacacaa
1201 acagctgcct caacccatgc tttatgtatccat ttcgttgc ttttgccttca
1261 gagaggcttgc tatcccaacc ttgcgttgc ttttgccttca
1321 agaacatctg agaccaccc tccacggcca atacagtggatca
1381 aaaatctggaa agcagaaaact gtcgttgc ctcacacccatgc
1441 caccaagctt agaaggccacc atgtatgtgg aagcagggttgc ttcacaaat gtgttaggagg
1501 ctctaaatttctt cttagaaatgttgc gtcacttttgc
1561 ctctgtctgc cacatttagag ggacagccaa aagtaatgtgg agcatttggaa
1621 tataccacac cggaggatgc agtttgc ttttgc
1681 gtatgtgaat tggatgtatccatcataaaatggatccat
1741 gcaaaatattt atgacatccaa caaagaagaa ccatcttttgc
1801 cataaaatgttgc atgtatccatc ttttgc
1861 ttttttgc
1921 tagcatctgg ctaaggccatc
1981 aataacatct cttcatctca
2041 tctgaaacac agtcatgtgt
2101 ccaaagatgc atcatgggg
2161 tc



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FIGURE 6A

SEQ ID NO:9

1 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcggtccc ctccgcctga
61 cgctcctctc tgtctcagcc aggactggtt tctgtaaagaa acagcaggag ctgtggcagc
121 ggcgaaaaggaa agcggtctgag ggcgttggaa cccgaaaagt ctgcgtgtc ctggctaccc
181 cgcacagcgg tgcccgcgg ggcgtcagta ccatggacag cagcgtgtcc cccacgaacg
241 ccagcaattg cactgatgcc ttggcgtact caagttgtc cccagcaccc agccccgggt
301 cctgggtcaa cttgtcccac ttagatggca acctgtccga cccatgcggg cccgaaaccgca
361 ccaacctggg cgggagagac agcctgtgcc ctccgacccgg cggcagtcctcc atgatcacgg
424 ccatcacatg catggccctc tactccatcg tttgtcggtt gggctcttc ggaaacttcc
484 tggtcatgta tgtgattgtc agatacacca agatgaagac tgcaccaac atctacattt
544 tcaaccttgc tctggcagat gccttagcca ccagtagccct gccttccag agtgtgaatt
604 acctaataatggg aacatggcca tttggaaacca tcctttgcaaa gatagtgatc tccatagatt
664 actataacat gttcaccaggc atattcaccc tctgcaccat gagtgttgcat cgatacattg
724 cagtcgtccca ccctgtcaag gccttagatt tccgtactcc ccggaaatgccc aaaattatca
784 atgtctgcaat ctggatccctc tcttcagcca ttggctctcc tggatgttc atggctacaa
844 caaaataacag gcaagggttcc atagattgtc cactaacatt ctctcatcca acctggtaact
904 gggaaaacccct cgtgaagatc tttgtttca ttttcgcctt cattatgcca gtgtcatca
964 ttaccgtgtc ctatggactg atgatcttgc gcctcaagag ttttcgcatg ctctctggct
1024 ccaaagaaaa ggacaggaat cttcgaagga tcaccaggat ggtgtgggtg ttgggtggctg
1084 ttttcatcgt ctgtggact cccattcaca tttacgtcat cattaaagcc ttgggttacaa
1144 tcccagaaac tacgttccag actgttttttgc ctttcgcctt cattatgcca ggttacacaa
1204 acagctgcct caaccaggatc tttatgcat ttctggatga aaacctcaaa cgatgcttca
1264 gagagttctg tatcccaacc tttccaaaca ttgagcaaca aaacctccact cgaattcgtc
1324 agaaeactag agaccacccc tccacggcca atacagtggta tagaactaat catcagctag
1384 aaaatctgga agcagaaaact gtcgcgttgc cctaacagggttgc ttttcgcctt
1444 caccaagctt agaagccacc atgtatgtgg aagcagggttgc tttcaagaat gtgttaggagg
1504 ctctaattctt cttagaaatgtt gctactttt aggtcatcca accttttcc ttttcgcctt
1564 ctctgctctg cacatttagag ggacagccaa aagtaagtgg agcatttggaa aggaaaggaa
1624 tataccacac cgaggagttcc agtttgcata agacacccag tggaaacccaa accatcgt
1684 gtatgtaat tgaagtcattc ataaaagggttgc ttttcgcctt ctttgcatttgc ttttgcatttgc
1744 gcaaatattt atgacactcaa caaagaagaa ccattttttgc ttaagttcact cgttagtaaca
1804 cataaagtaa atgctaccc ttttgcataat ttttgcataat ttttgcataat ttttgcataat
1864 ttttttgcataat ttttgcataat ttttgcataat ttttgcataat ttttgcataat ttttgcataat
1924 tagcatctgg ctaaggcatc attttcaccc ttttgcataat ttttgcataat ttttgcataat
1984 aataacatctt ctttgcataat ttttgcataat ttttgcataat ttttgcataat ttttgcataat
2044 ttttgcataat ttttgcataat ttttgcataat ttttgcataat ttttgcataat ttttgcataat
2104 ccaaagatc atcatggggg attttcatttgc ttttgcatttgc ttttgcatttgc ttttgcataat
2164 tc



600-1-266. FIGURE 6B

SEQ ID NO:10

Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
1 5 10 15
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val
20 25 30
Asn Leu Ser His Leu Asp Gly Asn Leu Ser Asp Pro Cys Gly Pro Asn
35 40 45
Arg Thr Asn Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Gly Ser
50 55 60
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
66 71 76 81
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
86 91 96
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
101 106 111
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val
116 121 126
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile
131 136 141
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu
146 151 156 161
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys
166 171 176
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys
181 186 191
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala
196 201 206
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser
211 216 221
His Pro Thr Trp Tyr Trp Glu Asn Leu Val Lys Ile Cys Val Phe Ile
226 231 236 241
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu
246 251 256
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu
261 266 271
Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
276 281 286
Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
291 296 301
Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
306 311 316 321
His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
326 331 336
Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
341 346 351
Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
356 361 366
Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
371 376 381
Thr Asn His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
386 391 396 401



Figure 7A

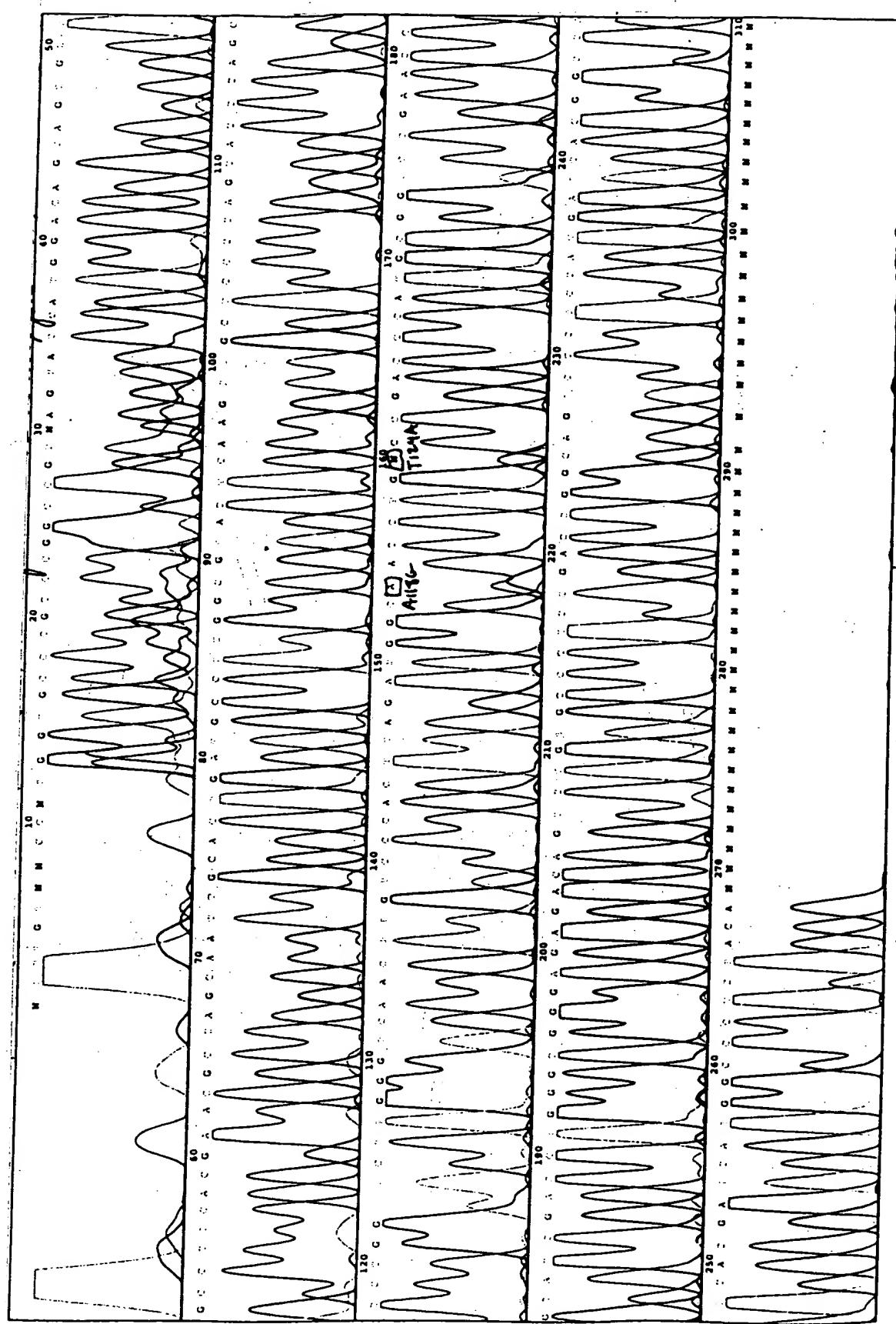




Figure 7B

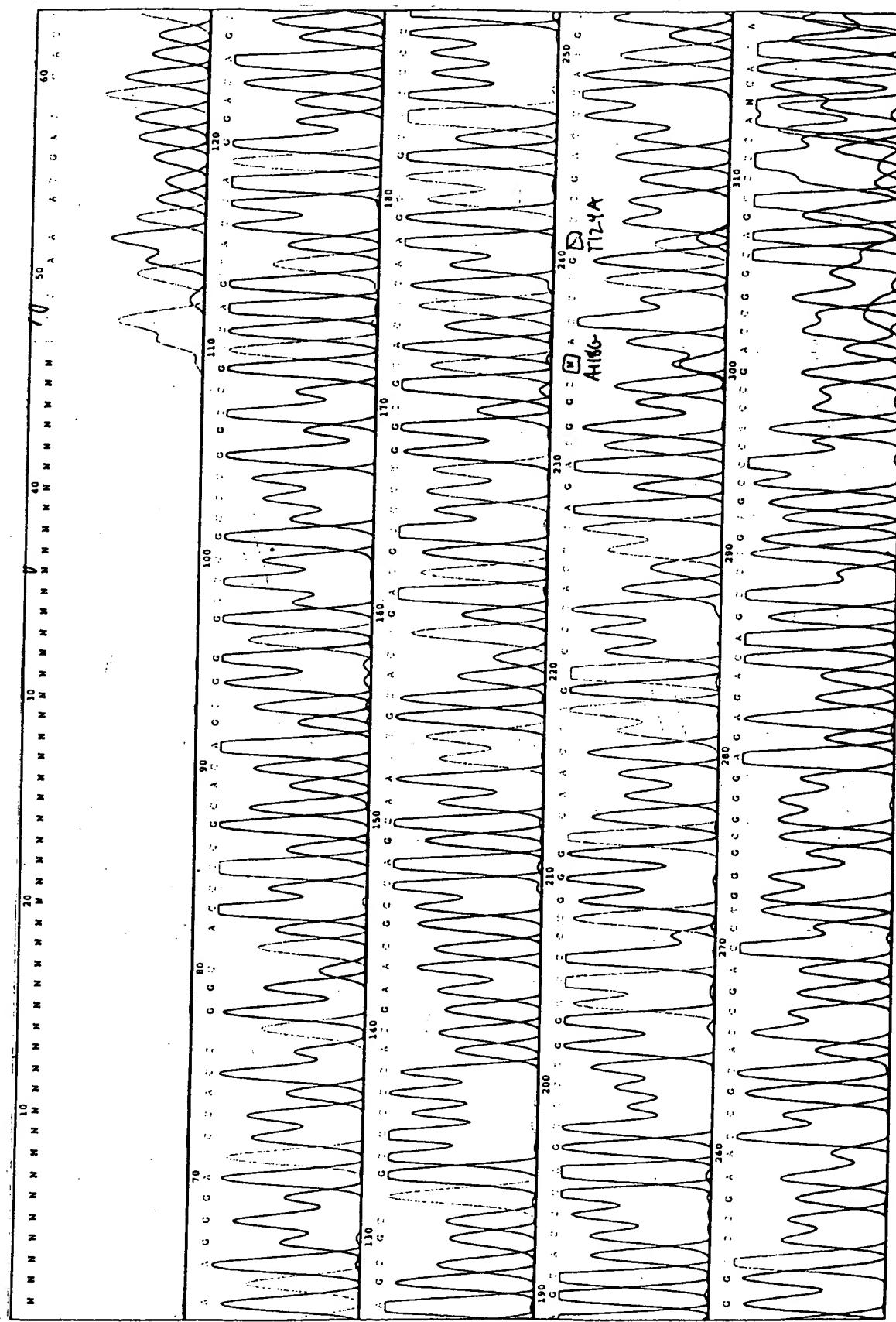




Figure 8A

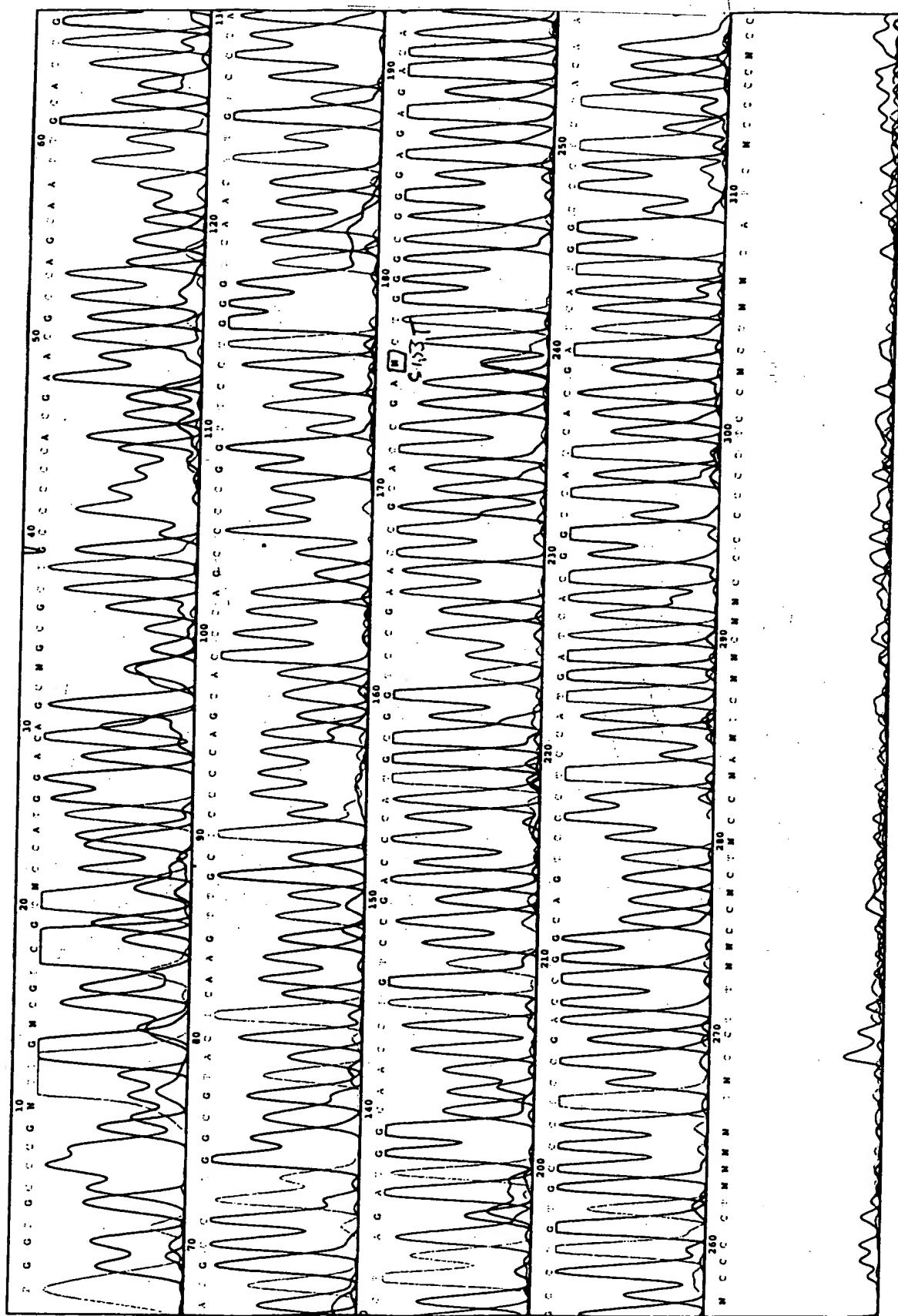


Figure 8B

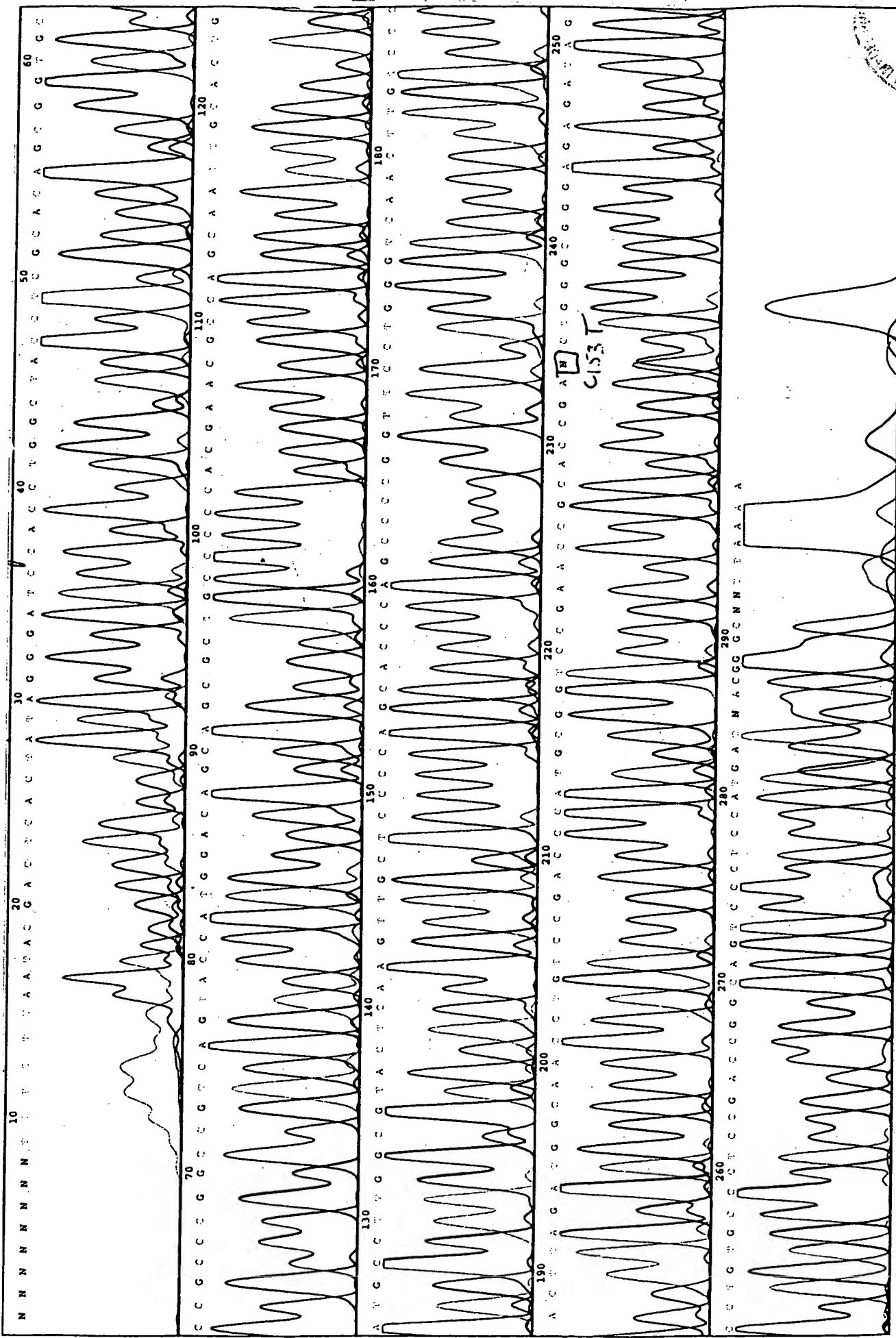




Figure 9A

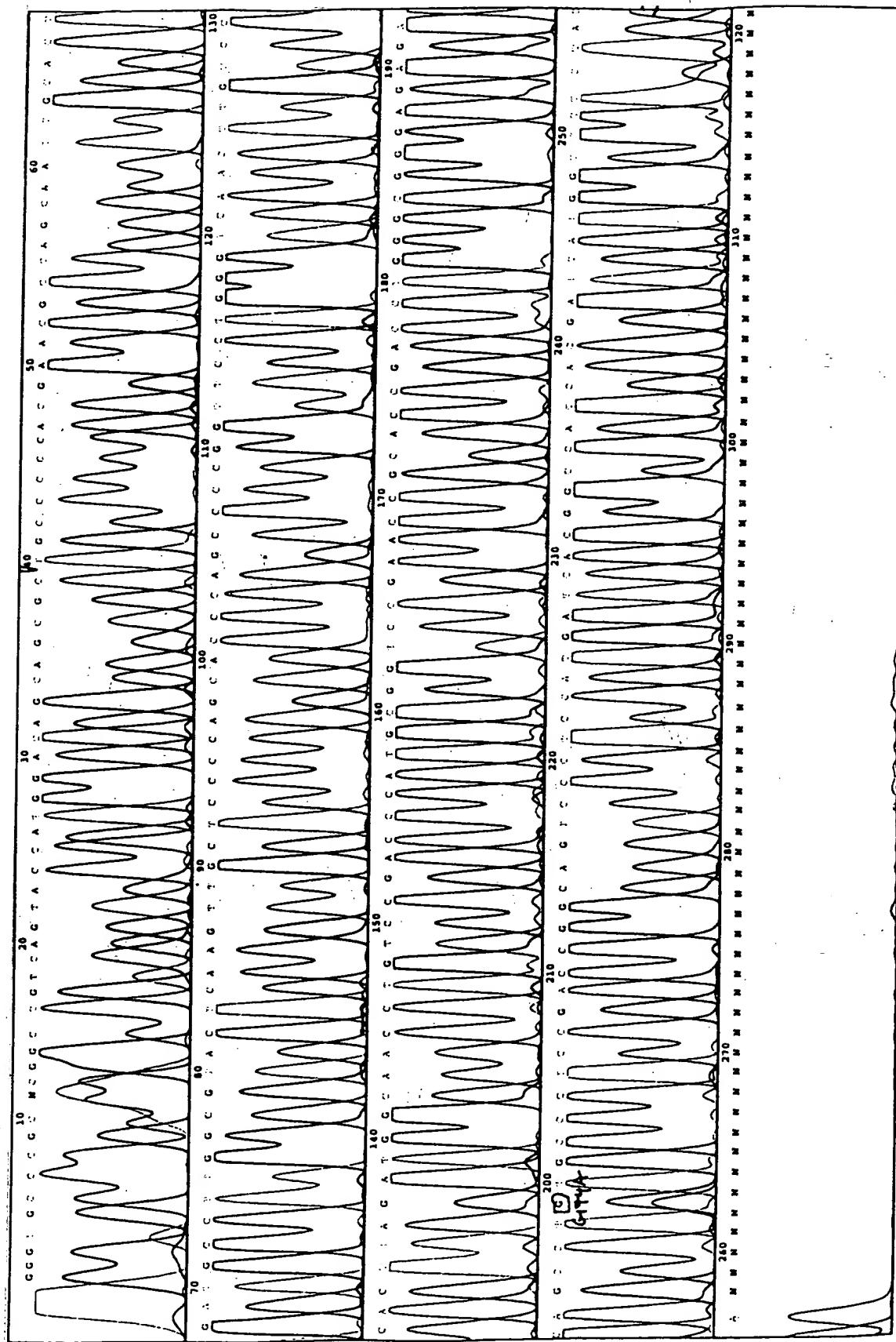




Figure 9B

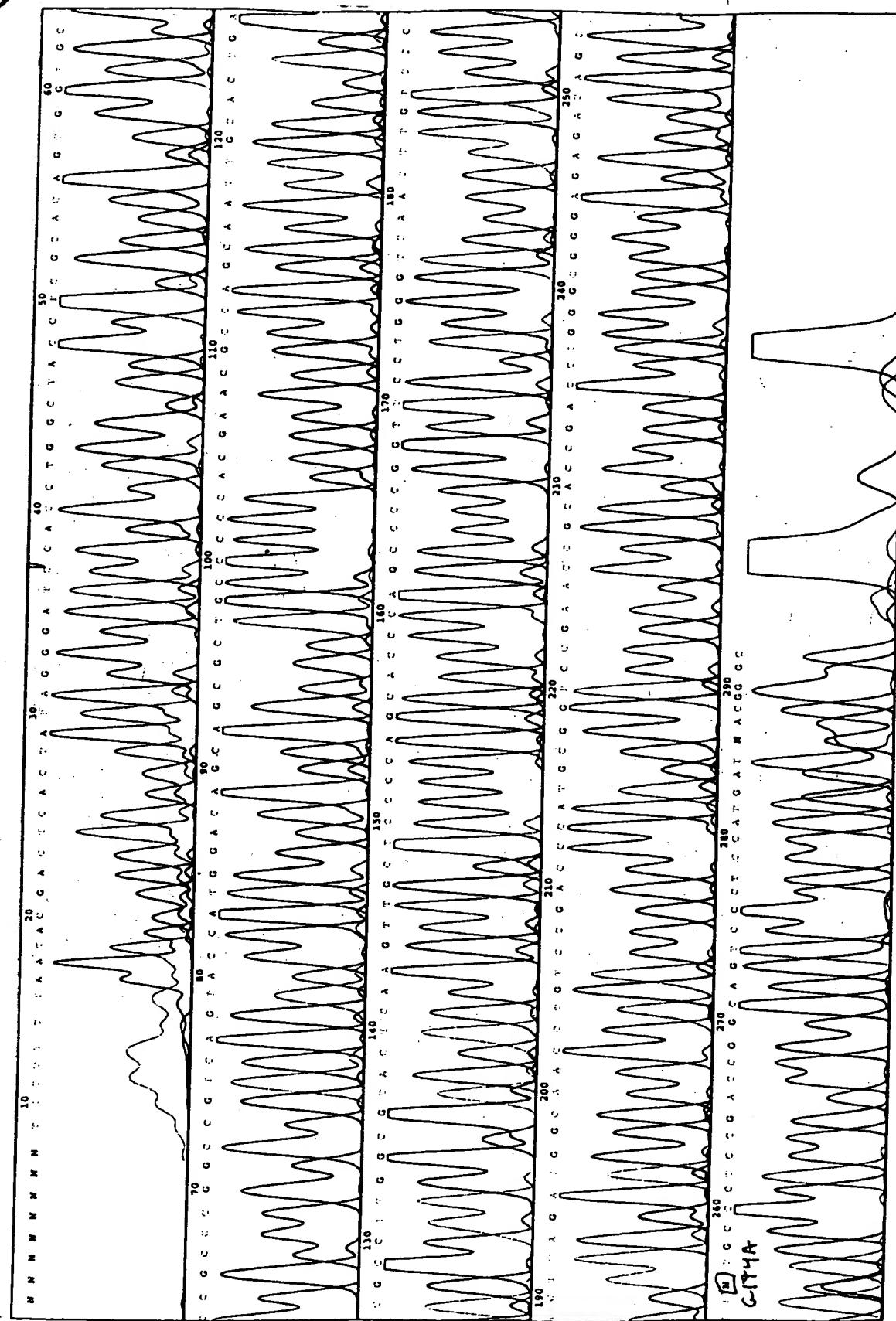




Figure 10A

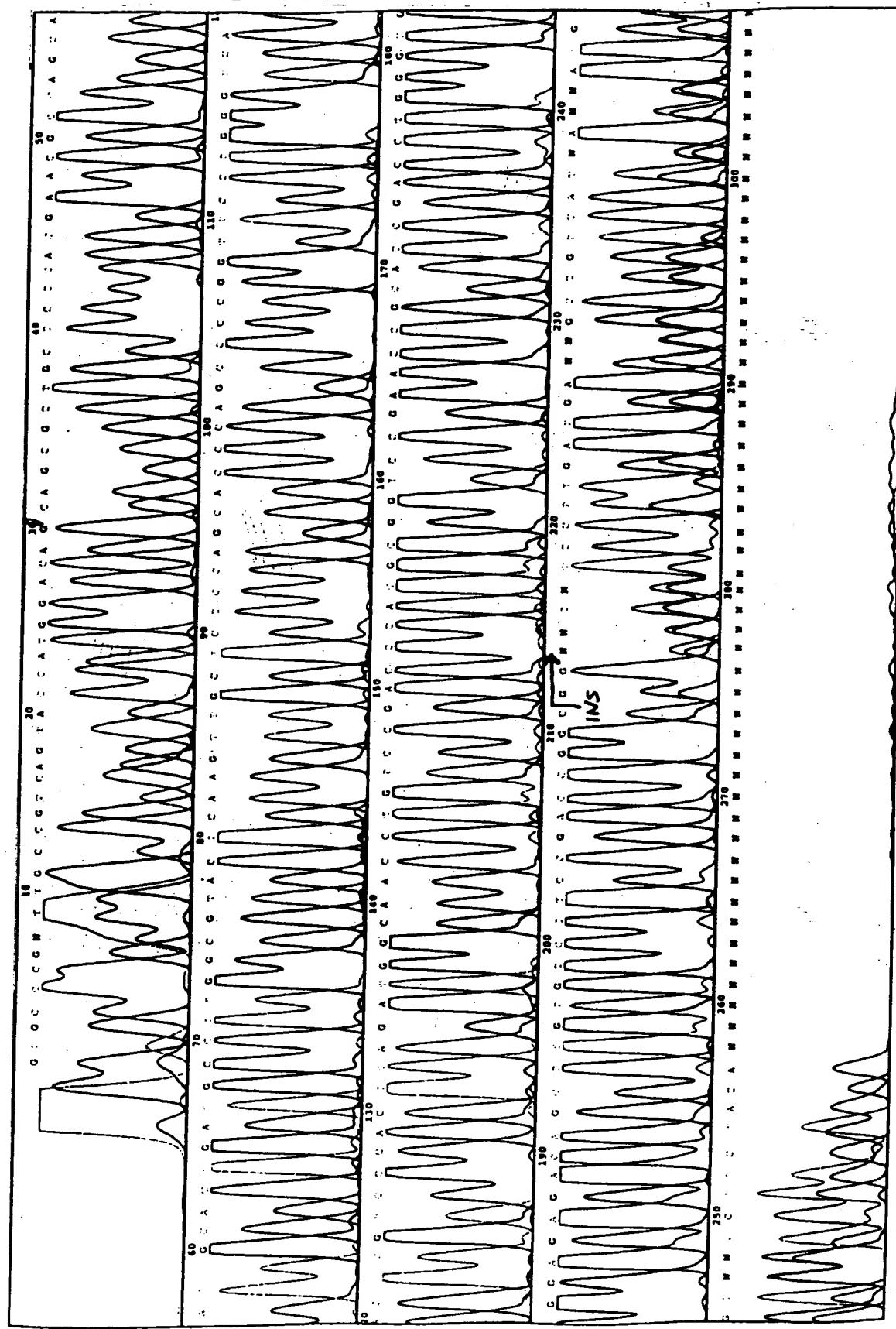




Figure 10B

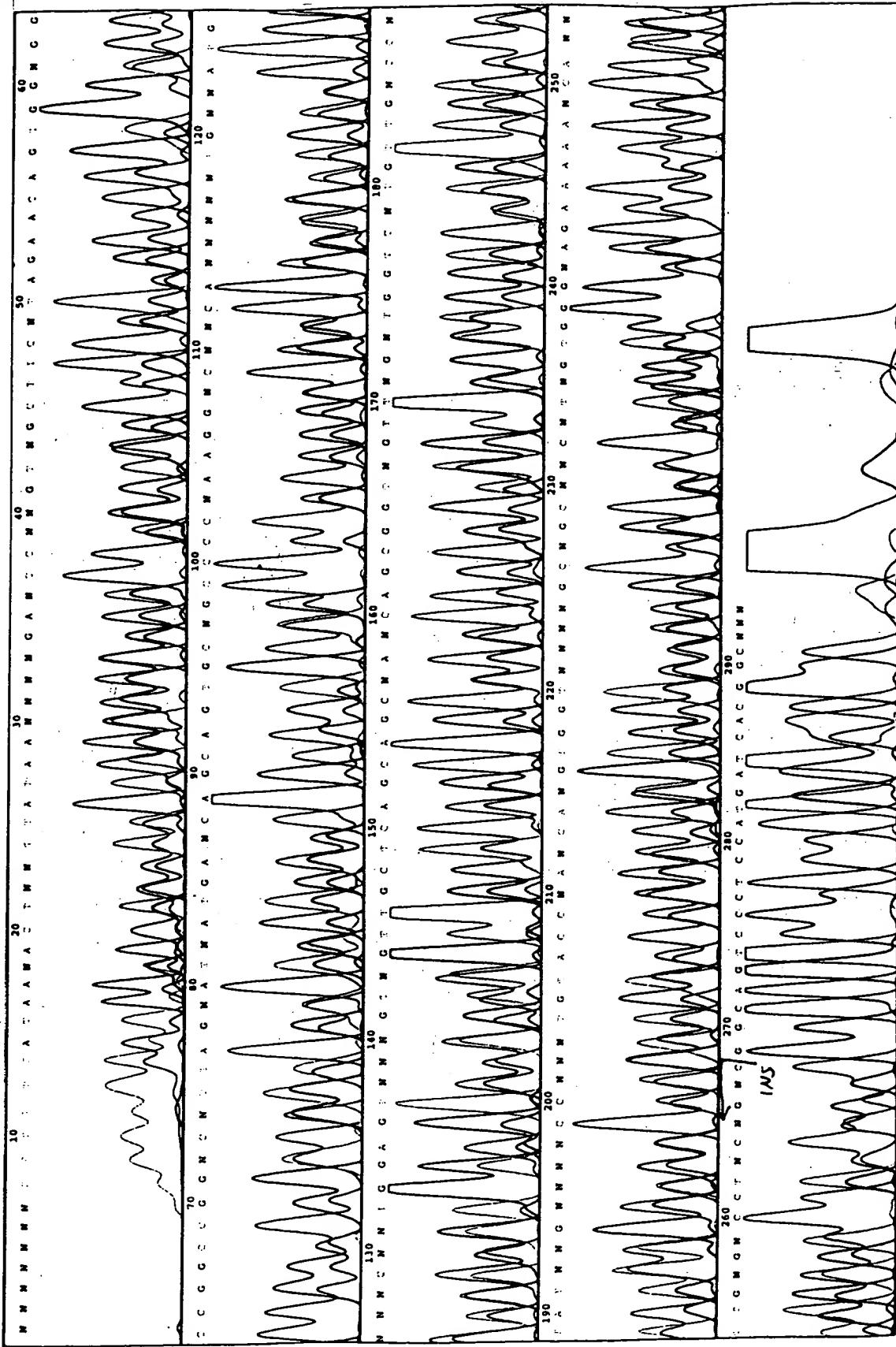




Figure 11A

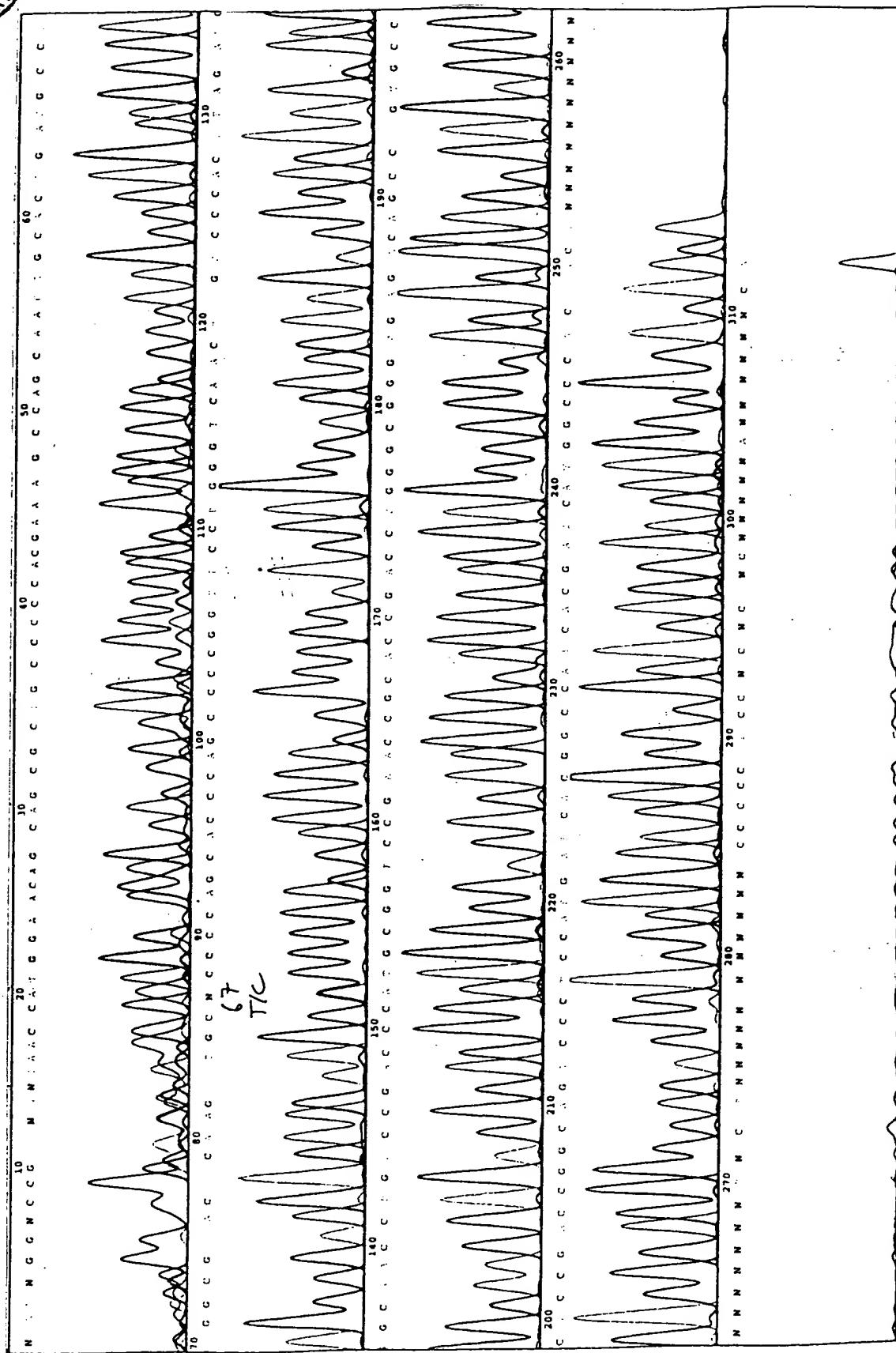




Figure 11B

